BI546216 603188602
BA791818 vs61c09.r
AL202756 Tetraodon
AC085155 Pen trog1
BI461092 603207340
AL16666 Tetraodon
BH681941 UT-E-EJI-BH681941 UT-E-EJI-BH681941 UT-E-EJI-BH681931 BB631937 BB633785 AL653785 BG71853 AL653785 AL6537815 BB15580 603027531 AL553294 AL553293 AL553293 AL553293 AL553293 AL553293 AL553293 AL553293 AL553393 AL553293 AL553233 AL53323 AL53323 AL533333 AL53333 AL533333 AL53333 AL533333 AL533333 AL53333 AL5

AQO87397 BF211581 BF211581 CNS03K4E AZ593746 AZ593785 BQ718536 A77923983 A1923983 A1923983 A1923983 A1831578 BR195029 BR195029 BR195029 ANS66092 AN

CNS02LFV AG085155 BI461092 CNS01TL3

H87640 BM683941 BM931807

BI546216 BI463670 AA791818

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Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810038K19:McLeod syndrome gene homolog, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK007734.1 GI:12841469
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 10 day old male pancreas cDNA to mRNA, clone lib:RIKEN full-length enriched mouse cDNA library clone:1810038K19.

Buka musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
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BC027097 Mus muscu
BB200527 BB200527
BG675952 G0262310
AL652777 AL652777
BB031611 130228 MA
                                                                                                                    March 30, 2003, 02:51:12 ; Search time 1672.99 Seconds (without alignments) 13446.329 Million cell updates/sec
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               GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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BM470447 AGENCOURT BM466219 AGENCOURT BI463669 603207339

BE735816 BM472443

ALIGNMENTS

2

JOURNAL MEDLINE

TITLE

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ITKKRQMPKDGLSEEVEKEVGQAEGKLITHRSAFSRASVIQAFLGSAPQLTLQLYITV
LEQNITTGREVERTHISLLSIYYGALBARKNILATKYDEXEVKWRLAVVCIFURRSFE
LAGNITGREVILVLYLFTKIWVVALILNRFFSPLYPMIVFWCSGSPFBRIEKALSRVGT
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/dev_stage="10 day old"
1. .1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MKFPASVIASVFLFVAETAAALYLSSTYRSAGDRMWQVLTLLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WYFFKTDIYMYVCAPLLILQLLIGYCTGILFMLVFYQFFHPCKKLFSSSVSESFRALL.
RCACWSSLRRKSSEPVGRIDTDLKACTEQDVMPTTSKVIPEATDIWTAVDLCSA"
         was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 TCCACCTITITGTACTGTGGGGGGGCTGCATCTGCTTTGTACATGGTTAGAATCTATCGA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 TCCGCAGGGGACCGCATGTGGCAGGTGCTGACGCTGCTCTTCTCCTTGATGCCCTGCGCC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 CTGCTCATGCACCTGCTCCAGCTCGGGCCCCTGTACAGGTGTTGTGAAGTCTTTTGTATC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 --GAAGATGCTAATAGATGGCGAGGAGGTGCTGATAGAATGGCAGGTGGGCCACTCCATC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="McLeod syndrome gene homolog
data source:MGD, source key:MGI:103569, evidence:ISS
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Pred. No. 6.7e-72;
0; Mismatches 491; Indels
                                                                                                                                                      /strain="C57BL/6J"
/db_xref="FARTOM DB:1810038K19"
/db_xref="MGD:MGT:1901251"
/db_xref="taxon:10090"
/clone="1810038K19"
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/db_xref="GI:12841470"
                                                                                                                                      organism="Mus musculus"
                                                                Location/Qualifiers
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/note="putative"
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/gene="Xkh"
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Best Local Similarity 55.6
Matches 630; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
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cDNA Library Preparation: Life Technologies, Inc
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/organism="Mus musculus"
/db_xref="taxon:10090"
/map="CZECH II"
/clone="IMAGE:5012421"
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1774 bp mRNA linear HTC 07-AUG-2002 Mus musculus, McLeod syndrome gene homolog, clone IMAGE:5012421,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1774)
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Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       945 AGCTICTICTIAIAICCCIGGAICGITITCIGGIGCAGGGCICCCCATICCTGAGAAC 1004
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                                                                                                                                                                     TGCAATATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTTGGGCCACTA 753
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                                                                                                                                                                                                                                                                                                                                                                                                          874 ATCATCCTCTTTGAGCCCTGGATTAAGTTCTGGAGAGTGGTGCCCAGATGCCCAATAAC 933
                                                                                                                               705 ACTGGAAGATGCTTCATCATGACCTTGTCCTGCTGTCTATTGTCTATGGCGCCTTACGT
                                                                                                                                                                                        GTGCTCTTCTCAGCCACTTTGAAATTGAAGCTGTGCCCTTCCTAGTGCTCAACTTCCTG
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                GGCTCAGTGCCCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCTGCAGAGGTTCCC
                                                    645 GGCTCTGCCCCACAACTGACCCTACAACTGTATATAACTGTCTTGGAGCAGAACATCACT
                                                                                           634 CTGGGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCCACCCTT
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Lint. at: http://image.llnl.gov Series: IRAK Plate: 45 Row: d Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: marched mRNA gi: 12963702 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NCI_CGAP_Lu29" /lab_host="PH10B" /lab_host="PH10B" /lab_host="Vector: pCMV-SPORT6" s13 c 441 g 434 t
                                                                                                                                                                                                                  Contact: amg@bcm.tmc.edu
donaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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21.2%; Score 294.6; DB 11; Length
Best Local Similarity 55.7%; Pred. No. 1.8e-69;
Matches 631; Conservative 0; Mismatches 489; Indels
                                                                                                                             Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases I to 624)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,

Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y. Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. et al. 2001)

I Unpublished (2001)

On Jun 30, 2000 this sequence version replaced gi:8865480.
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Tel: 81-45-503-9222
Pax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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The Institute of Physical and Chemical Research (RIKEN)
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793 TGCAACATCTTAGCCATCAAATCAAGTATGATGAGTATGAGGTCAAAGTCAAACCCCTG 852
                                                                                                                               GCTTATGTCTGTATCTTCCTCTGGAGAGCTTTGAGATTGCCACCCGAGTCATCGTCCTC 912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
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Encyclopedia Project of Genome Exploration Research Group in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Location/Qualifiers
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/clone="A430025D09"
/clone_lib="RIKEN full-length enriched, 0 day neonate
thymus"
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0; Mismatches 16; Indels
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/dev_stage="0 day neonate"
/lab_host="DH108"
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/organism="Mus musculus"
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60262310F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4747323 5',
mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Londott: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
Contact: Brocurement: James Cleaver, M.D.
Contact: Robert Strayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
clone distribution: G.E. Consortium/LLNL at:
http://image.llnl.gov
row: column: 04
High quality sequence strat: 4
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/clone="IMAGE:4747323"
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/clone="IMAGE:4747323"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/note: pcm, Vector: pcm, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Vertage, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 810)
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                                                       544 AAACGTATGTCACAGATCCAAGCCTTCCTGGGCTCAGTGCCCCAGCTGACCTATCAGCTC 603
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17.8%; Score 247; DB 12; Length 810;
Best Local Similarity 99.6%; Pred. No. 1.5e-56;
Matches 258; Conservative 0; Mismatches 0; Indels
                                                                                                                                               TATGTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTG 648
                                                                                                                                                                                      1. .810
/organism="Homo sapiens"
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AUTHORS
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Email: trop@sanger.ac.uk
Sanger Xenpous tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas029g15.sp6
Sequencing primer: $P6
Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL652777 AL652777 XGC-gastrula Silurana tropicalis cDNA clone TGas029915 5',
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Sukaryota, Metazoca, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Silurana
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                           246 CTTTTGCCTTGGGTTAAATTCTGGAGCAGTGGGGACAGCCTGCCCCAAAACATAGAAAG 305
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Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001)

Unpublished (2001)
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Pred. No. 8.1e-55;
0; Mismatches 269; Indels 0;
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Best Local Similarity 59.9%;
Matches 402; Conservative (
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                                                                        1110 GGTAGAGAATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAA 1169
                                                                                                                                                                 1170 TIACTGTCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTT 1229
                                                                                                2 GGTAGAGAACGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTACTGGA
                                                                                                                                                                                             THACTGTCATTCCTCGATTGCTTTGCAGCTCATTATTGCTTACCTGATTTCCATTGGCTT
                                                                                                                                                                                                                                                                                      122 CATGCTCCTTTTCTTCCAGTACTTGCACCCGCTGCGCTCACTCTTCACCCACAACGTAGT
                                                                                                                                                                                                                                                                                                                                                     1290 AGACTACCTCCATTGTGTCTGCTGTCACCAGCACCCTCGGACCAGGGTTGAGAACTCAGA
  Pred. No. 2.6e-54;
                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence. _ _ BI827782
BI827782
BI827782.1 GI:15939332
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56.8%;
90.7%;
                            Matches 254; Conservative
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Best Local Similarity
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Best Local Similarity
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KEYWORDS
SOURCE
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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                                                                                                                                                                                                                 62
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TITLE
JOURNAL
COMMENT
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BI827782
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 09-JUL-2000
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1 (bases 1 to 392)
1 The Strong S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall;
Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                                                                                                                    1123 ATCATGGTCTTGGTTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCC 1182
                                                                                                                                                                                                                                                                                                                               1183 TTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCTCCTTTTC 1242
                                                                                                                                                                                                                                                                                                                                                                                                                           1243 TTCCAGTACTTGCATCCATTGCGCTCACTCTTCACCCATAATGTAGTAGACTACCTCCAT 1302
                                                                                                                                           1063 AAAGGGCAGAACTGGGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTG 1122
  306 AACTTTAGCTGGTTTGGTACTGTGACAGTCCTTGGGTCAGTAACCTTGCTTTATTCAGCC 365
                                                                                             366 AFCAATATGTTTTGCTGTCTGCTGTTCAGCTAAACCTATCAGATCGGGACTTAATTGAC 425
                                                                                                                                                                                      426 CAGTCACAAAACTGGGGGAGGTTAAGTCTTTATACCATTCGGTTGCTCGAGAATGCA 485
                                                                                                                                                                                                                                                                                  486 GCCCTCATTCTGCTCTGGTACTTCTACAAGGAGGATGTGTTTGAGTATTTCTGTTCCCCA 545
                                                                                                                                                                                                                                                                                                                                                                             546 CTGCTGGTGGTTCAACTCTTAGTAGGATATGCCACCGCCATCTTCTTCATGCTGCTTTTT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 TACCAGTACCTTCACCCTTGCCGCTTCCTTTTCAGCCACAACGTTGAAGACTGTTTGGCT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 238.4; DB 10; Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE031611 392 bp mRNA linear 130228 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 59 row. C column: 17
Seg primer: ATTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT
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EST.
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Sus scrofa
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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BE031611
LOCUS
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B1827782 881 bp mRNA linear EST 04-OCT-2001
603075458F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5167070 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpretation Drain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECGRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT prinned and directionally cloned (ECGRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.93 kb. Library is normalized and enriched for full:length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (Dases 1 to 881)
Nat-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Lncyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM11415 row: d column: 15

High quality sequence stop: 782.

Location/Qualifiers
182 GGACTACCTACACTGTGTGTGCTGCCATCAGCACCCTCGGGGCAGGGTTGAGAACTCAGA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 206.2; DB 13; Length 881; Pred. No. 2.5e-45;
                                                                                GCCACCCTTTGAGACTGAAGCAAGGCAAAGTGTTGTCTGA 1389
                                                                                                                                                                242 GCCATCTGTTGATGCTGAACAAGGCAGAGCATTGTCTGA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Invitrogen). Kesealum cunchis is a NIH MGC Library."
163 c 194 g 266 t
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db_xref="taxon:9606"
clone="IMAGE:5167070"
clone lib="NIH MGC 119"
/tissue type="medulTa"
/lab_host="DH10B"
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/ organism="Homo sapiens"
/db_arzef="taxon:9606"
/clone="ImAGE:686506"
/clone="ImAGE:686506"
/clone="Imb="NGI_CGAP_GGB1"
/tissue_type="germinal center B cell"
/lab_host="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and clonned into the Not I and Eco RI sites of the modified pTTM3 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL638533 XGC-neurula Silurana tropicalis cDNA clone TNeu018n12 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1235
                                                                                                                                                                                Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1241 Std Brror: 0.00
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 183.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1116 GAATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTG 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1236 CCTTTTCTTCCAGTACTTGCATCCATTGCGCTCACTCTTCACCCATAATGTAGTAGACTA 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAATGTGATCATGGTCTTGGTTTTTAAGTTCTATGGAGTGAAAGTGTTACTGAATTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1176 TCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCATTCCTTGATTGCCTTGCACTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCT
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                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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                                                                                                                      Tumor Gene Index
Unpublished (1997)
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AL638533
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EST.
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AL638533/c
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ORIGIN
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AUTHORS
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Zaggoof.rl NCI_CGAP_GCBl Homo Baplens CDNA clone IMAGE:686506 5',
                                                                                                                                                                                                                                                                                                                                                                  271
                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                            128 GATTTACTTTTCCATTTAGCATCCTTTTCTCCCACCTTTTTGTACTGTGGGGAGGCTGCAT 187
                                                                                                                                                                                                                                                                     152 Archadcririccririndcarrarcrirchaacrerichacrerderenderender 211
                                                                                                                                                                                                                                                                                                                 188 CTGCTTTGTACATGGTTAGAATCTATCGAAAGAATAGTGAAACTTACTGGATGACATACA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccarcagcirrariarirgisesescaarirrissarcaaarrarccigarerirricaaca 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGATCTAGCCAAAGATAAACCGCTATCATTATTATGCATCTAATCCTCTTGGGACCTG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 AGGAGCCCTATGTCAGCCTCACCCGAAAGAAGATGCTAATAGATGGCGAGGAGGTGCTGA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAGGAAGACTCAAGTTAGCATCACAAAGAG--------AAACACGATGC 496
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                                                                                                                                                                             93 Aagaaagacacaggagariricarcircgaaagaagaaragiccrigg-cagagacrcc 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INGIGAGGIGITIGCACACCATTAGAATTACCACAAATGGTTGAAAAATCTTAAACAGG 451
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    19; Gaps
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                                                                                          CAAGGAAGCAAGAAAAATAAGCACCCTGAGAATGGAGACAGTGT-TGAAGAGATGGATG 92
                                              CAAGACCACAACATTCAGAAAGAACCTCGACAATGGACAGAGTTTATGAAATTCCTGAGG
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                                                                                                                                                                              Hinkton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE 1D: TNeu018112.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Asron M. Zorn.
Location/Qualifiers
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Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
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RESULT 10

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
E. (Dases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
L. Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Miklos J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninoi (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11655 row: c column: 02
High quality sequence stop: 707.
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/note="Organ: brain, Vector: pBluescriptR (modified force="Organ: brain, Vector: pBluescript KS+); Site 1: BamH1; Site 2: Sall-XhoI (gtcgag) pBluescript KS+); Site 1: BamH1; Site 2: Sall-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', slze-selected for average insert size 2:5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (INMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
603188602F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5259961 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI463670 855 bp mRNA linear EST 21-AUG-2001
603207340F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5273312 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   945 CTICAGCCGGGICGCACTCTGGIGGICCTGATTTCAGICACCATCCTCTATGCTGGCAT 1004
                                                                   646 GTGCTAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTG 705
                                                                                                                         764
                                                                                                                                                                                                                                         412 GCCATCAAAATCAAGTACGATGAGTATGAGTCAAGAGTGAAGCCTCTGGCCTATGTCTG 471
                                                                                                                                                                                                                                                                                                                   824
                                                                                                                                                                                                                                                                                                                                                                         472 TATCTTCCTGTGGAGGAGCTTTGAGATTGCCACTCGAGTTGTAGTCCTGGTCCTCTTTAC 531
                                                                                                                                                                                                                                                                                                                                                                                                                                   825 AGCCACTITGAAATIGAAGGCTGTGCCCTTCCTAGTGCTCAACTICCTGATCATCTCTT 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 crccgrcrcanaccrcaccaccrcaranaracrcarcacrrcrrcacrrrrrrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             885 TGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCCAATAACATTGAGAAAAA 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 graccccrddarccrcrircrdcrdcrdcrdcrcccarrcccrdadardradad-aage 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651 CCTCAGTAGAGTGGGCACCATTGTACTATGCATTCTAACTTTACTCTATACTGGGTA 710
292 CAGCTGACCCTACAGCTGTACATAAGTGTCATGCAGCAGGACGTCACTGTTGGAAGAAGT 351
                                                                                                                                                                                      706 GCTATCCAGATCAAGTACGATGACTAC-AAGATTCGCCTTGGGCCACTAGAAGTCCTCTG
                                                                                                                                                                                                                                                                                                         765 CATCACCATCTGGCGGACATTGGAGATCACTTCCCGGCTCCTGATTCTGGTGCTCTTCTC
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/db xref="taxon:9606"
/clone="ImaGE:527312"
/clone lib="WHH MGC_97"
/lab_host="DH10B"
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B1463670
B1463670.1 GI:15254326
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Marray.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ארוו בארון בארון מאראים 185 bp mRNA linear EST 09-FEB-1996 vs61c09.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1150768 5' similar to SW:XK_HUMAN P51811 MEMBRANE TRANSPORT PROTEIN XK ;, mRNA sequence.
Institutes of Health). Note: this is a NIH_MGC Library." 156 c 186 g 256 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCCAAATGTGGATCCGGTTTCATCTCTGGAGGAAGATGTCATCCGTGGAGCCAACCCCC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AAGAAAGCACAGGAGGAGTTTCATCTTCGAAAGAAAATAGTCCTTGGCCAGAGACTCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 AAGACTTGAGGAGAAATAAGGCTGCATTACTTTTTTGGCACATTCTTCTTTTAGGACCTA 431
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                                                                                                                                                                                                                                                                                              8 CAAGACCACAACATTCAGAAAGAACCTCGACAATGGACAGAGTTTATGAAATTCCTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 GGCAAAGGGAGATTGCATTCTCAATCCGGGATAATTTCATGCAGCAGAAGGCTTTCAAGT
                                                                                                                                                                                                                          14;
                                                                                                                                                      DB 13; Length 855;
                                                                                                                                               Score 174.2; DB 13; Length
Pred. No. 1.5e-36;
0; Mismatches 248; Indels
                                         186 9
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us-09-768-781-2.rst

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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.ft/Tetraodon.
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                             Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
                                                                                        2 (bases 1 to 691)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="G"
/note="Genoscope sequence ID : COAG147BE08LP1~end : T7"
182 c 187 g 189 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 TGCTCTTCTTCTTCCAACCCTGGACCGAGTTCTGGGCCAAGAAAGGCTCGTTGACTC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            929 ATAACATTGAGAAAACTTCAGCCGGGTCGGCACTCTGGTGGTCCTGATTTCAGTCACCA 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AGGGCCTGGAGCGAAACTTCTCTCATTTCGGCACCGTGGTGGTGCTGAGCCTGTTCACGC 496
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Pred. No. 1.5e-35;
2; Mismatches 210; Indels
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    .691
    /organism="Tetraodon nigroviridis"
| db xref="taxon:99883"
| clone="147116"

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          Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-APR-2000)
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58.9%;
                                                                                                                                                                                                                                  (bases 1 to 691)
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Best Local Similarity 58.9
Matches 305; Conservative
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                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:623976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACCCTGGCTATGCACCGCAATGCCTACAAACGTATGTCACAGATCCAAGCCTTCCTGG 574
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The WashU-HHMI Mouse EST Project Unpublished (1996)
Contact: Marxa MyNouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forcet Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 173.2; DB 9; Length 385;
Pred. No. 2.1e-36;
0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       relone="IMAGE:1150768"
/clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                               Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 378.
Location/Qualifiers
1. .385
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                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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AUTHORS REFERENCE

TITLE JOURNAL

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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1. .666
| organism="Homo sapiens" |
| decoration="Homo sapiens" |
| decoration="INAGE:5272840" |
| clone="INAGE:5272840" |
| clone="INAGE:5272840" |
| decoration="Selection of the control of the contro
                                               BI461092 666 bp mRNA linear EST 21-AUG-2001
603206970F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272840 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.hib.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
TobNA Library Preparation: Michel J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11688 row: k column: 17
High quality sequence stop: 663.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (base 1 to 66) NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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BI461092.1 GI:15251748
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Biract Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesegger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tal:81-45-503-9111, Fax:81-45-503-9170,

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                           Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Pan troglodytes DNA, clone: PTB-083B22.F, genomic survey sequence
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                   clone_lib:PTB Chimpanzee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          880 CTCTTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                       Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
151 c 127 g 181 t 2 others
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                                                                                                                                                              Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-083B22.F.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A., T
TotoKi,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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/organism="Pan troglodytes"
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/clone="PTB-083B22.F"
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